

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/529,349  
Source: PG  
Date Processed by STIC: 2/9/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 02/09/2006

PATENT APPLICATION: US/10/529,349

TIME: 12:31:08

Input Set : A:\P1988R1 Sequence Listing.txt

Output Set: N:\CRF4\02012006\J529349.raw

3 <110> APPLICANT: Bodary-Winter, Sarah C.  
 4 Clark, Hilary  
 5 Jackman, Janet K.  
 6 Schoenfeld, Jill R.  
 7 Williams, P. Mickey  
 8 Wood, William I.  
 9 Wu, Thomas D.  
 11 <120> TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of  
 Psoriasis  
 13 <130> FILE REFERENCE: P1988R1-US  
 15 <140> CURRENT APPLICATION NUMBER: US 10/529,349  
 16 <141> CURRENT FILING DATE: 2005-03-25  
 18 <150> PRIOR APPLICATION NUMBER: PCT/US03/027382  
 19 <151> PRIOR FILING DATE: 2003-08-28  
 21 <150> PRIOR APPLICATION NUMBER: US 60/414,484  
 22 <151> PRIOR FILING DATE: 2002-09-26  
 24 <160> NUMBER OF SEQ ID NOS: 48  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 3192  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Homo sapiens  
 31 <400> SEQUENCE: 1  
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 36 cccatactca gtagccaaga tggaggatgat gaacctgatg gagcagccta 150  
 38 tcaagggtgac tgagtggcag cagacataca cctacgactc gggatatccac 200  
 40 tcgggcgcga acacctgcgt gccctccgtc agcagcaagg gcatcatgga 250  
 42 ggaggatgag gcctgcgggc gccagtacac gctcaagaaa accaccactt 300  
 44 acacccaggg ggtgcccccc agccaagggtg acctggagta ccagatgtcc 350  
 46 acaacagcca gggccaaaacg ggtgcgggag gccatgtgcc ctggtgtgtc 400  
 48 aggcgaggac agctcgcttc tgctggccac ccagggtggag gggcaggcca 450  
 50 ccaacctgca gcgactggcc gagccgtccc agctgctcaa gtcggccatt 500  
 52 gtgcatctca tcaactacca ggacgatgcc gagctggcca ctgcgcct 550  
 54 gcccgagctc accaaactgc tcaacgacga ggacccgggtg gtggtgacca 600  
 56 aggcggccat gattgtgaac cagctgtcga agaaggaggc gtcgcggcgg 650  
 58 gccctgatgg gctcgcccca gctggtggcc gctgtcgtgc gtaccatgca 700  
 60 gaataccagc gacctggaca cagcccgtcg caccaccagc atcctgcaca 750  
 62 acctctccca ccaccgggag gggctgctcg ccatcttcaa gtcgggtggc 800  
 64 atccctgctc tgggtccgcat gctcagctcc cctgtggagt cggtcctgtt 850  
 66 ctatgccatc accacgtgc acaacctgct cctgtaccag gagggcgcca 900  
 68 agatggccgt gcgcctggcc gacgggctgc aaaagatggt gcccctgctc 950  
 70 aacaagaaca accccaagtt cctggccatc accaccgact gcctgcagct 1000  
 72 cctggcctac ggcaaccagg agagcaagct gatcatcctg gccaatggtg 1050  
 74 ggccccaggc cctcgtgcag atcatgcgta actacagtta tgaaaagctg 1100

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78 taagcctgcc attgtggagg ctggtgggat gcaggccctg ggcaagcacc 1200
80 tgaccagcaa cagccccgc ctggtgcaga actgcctgtg gacctgcgc 1250
82 aacctctcag atgtggccac caagcaggag ggcttgaga gtgtgctgaa 1300
84 gattctggtg aatcagctga gtgtggatga cgtcaacgtc ctcacctgtg 1350
86 ccacgggcac actctccaac ctgacatgca acaacagcaa gaacaagacg 1400
88 ctggtgacac agaacagcgg tgtggaggct ctcacccatg ccatcctgcg 1450
90 tgctggtgac aaggacgaca tcacggagcc tgccgtctgc gctctgcgcc 1500
92 acctcactag ccgccacct gaggcgaga tggcccagaa ctctgtgcgt 1550
94 ctcaactatg gcatcccagc catcgtgaag ctgctcaacc agcccaacca 1600
96 gtggccactg gtcaaggcaa ccatcggtt gatcaggaat ctggccctgt 1650
98 gcccagccaa ccatgccccg ctgcaggagg cagcggtcac cccccgcctc 1700
100 gtccaactgc tgggtgaaggc ccaccaggat gcccagcgcc acgtagctgc 1750
102 aggcacacag cagccctaca cggatggtgt gaggatggag gagattgtgg 1800
104 agggctgcac cggagcactg cacatcctcg cccgggaccc catgaaccgc 1850
106 atggagatct tccggctcaa caccattccc ctgtttgtgc agctcctgta 1900
108 ctcgctcgggtg gagaacatcc agcgcgtggc tgccggggtg ctgtgtgagc 1950
110 tggcccagga caaggaggcg gccgacgcca ttgatgcaga gggggcctcg 2000
112 gccccactca tggagttgct gcactccgc aacgagggca ctgccaccta 2050
114 cgctgctgcc gtccgtttcc gcatctccga ggacaagaac ccagactacc 2100
116 ggaagcgcgt gtccgtggag ctcaccaact ccctcttcaa gcatgacctg 2150
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120 agatgacatg gatgccacct accgccccat gtactccagc gatgtgcccc 2250
122 ttgacctgct ggagatgcac atggacatgg atggagacta ccccatcgac 2300
124 acctacagcg accgctcag gccccgtac cccactgcag accacatgct 2350
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128 tgcaggcgat ggggcaagac agaaaagtgc ctgagctggg gaagccgggg 2450
130 tgtaacttcc tgetgcaccc tgcgcctcca gaggtcctcc gtagggctct 2500
132 tcttgggata gtgttctgct cctgcttttc tgtcctgggc atgggtccag 2550
134 ggccctgacac cccctccccg cccctgtggc cctggccact aaagcttcag 2600
136 actcaagtac ccattctgtt ttcccccagc aacgccccctc caaacctcca 2650
138 gcctccctgt ctccagctgc ctgggccccg aagggttttg gttccttctc 2700
140 tgggtctgat tttctcactg aactccaccg accaactgcc ctaagcccc 2750
142 agggcctcca gggcccaggc tcgagaccca aacccccaaa atccaaaact 2800
144 tctcttgaaa agttcagggg ccgtccaggg gagatgggga ggagatatgg 2850
146 agtgagtcac ctgctccaga agatgccagc ttctctctcc aggggtgctta 2900
148 gttggctttg cccacccctc actccccagg gagctccggg gacagcttcc 2950
150 tcacacccct gtcccaccca cacagctgcc ctagctgacc ccgagaagtg 3000
152 ctcttggtg acccctctgg tgtgtggtga ggggctttct cttccccctc 3050
154 ctgtttcaga cccccccatt tccgcacat ggtgtggggg gctgggggag 3100
156 gtccaagcag agtgttttat tattatcgct ttatgttttt ggttatttgt 3150
158 ttttttgtat agaccaaagc aaagaaaata aaaataacac ag 3192
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 745
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 2
166 Met Glu Val Met Asn Leu Met Glu Gln Pro Ile Lys Val Thr Glu
167 1 5 10 15

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Input Set : A:\P1988R1 Sequence Listing.txt

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169	Trp	Gln	Gln	Thr	Tyr	Thr	Tyr	Asp	Ser	Gly	Ile	His	Ser	Gly	Ala
170				20						25					30
172	Asn	Thr	Cys	Val	Pro	Ser	Val	Ser	Ser	Lys	Gly	Ile	Met	Glu	Glu
173				35						40					45
175	Asp	Glu	Ala	Cys	Gly	Arg	Gln	Tyr	Thr	Leu	Lys	Lys	Thr	Thr	Thr
176				50						55					60
178	Tyr	Thr	Gln	Gly	Val	Pro	Pro	Ser	Gln	Gly	Asp	Leu	Glu	Tyr	Gln
179				65						70					75
181	Met	Ser	Thr	Thr	Ala	Arg	Ala	Lys	Arg	Val	Arg	Glu	Ala	Met	Cys
182				80						85					90
184	Pro	Gly	Val	Ser	Gly	Glu	Asp	Ser	Ser	Leu	Leu	Leu	Ala	Thr	Gln
185				95						100					105
187	Val	Glu	Gly	Gln	Ala	Thr	Asn	Leu	Gln	Arg	Leu	Ala	Glu	Pro	Ser
188				110						115					120
190	Gln	Leu	Leu	Lys	Ser	Ala	Ile	Val	His	Leu	Ile	Asn	Tyr	Gln	Asp
191				125						130					135
193	Asp	Ala	Glu	Leu	Ala	Thr	Arg	Ala	Leu	Pro	Glu	Leu	Thr	Lys	Leu
194				140						145					150
196	Leu	Asn	Asp	Glu	Asp	Pro	Val	Val	Val	Thr	Lys	Ala	Ala	Met	Ile
197				155						160					165
199	Val	Asn	Gln	Leu	Ser	Lys	Lys	Glu	Ala	Ser	Arg	Arg	Ala	Leu	Met
200				170						175					180
202	Gly	Ser	Pro	Gln	Leu	Val	Ala	Ala	Val	Val	Arg	Thr	Met	Gln	Asn
203				185						190					195
205	Thr	Ser	Asp	Leu	Asp	Thr	Ala	Arg	Cys	Thr	Thr	Ser	Ile	Leu	His
206				200						205					210
208	Asn	Leu	Ser	His	His	Arg	Glu	Gly	Leu	Leu	Ala	Ile	Phe	Lys	Ser
209				215						220					225
211	Gly	Gly	Ile	Pro	Ala	Leu	Val	Arg	Met	Leu	Ser	Ser	Pro	Val	Glu
212				230						235					240
214	Ser	Val	Leu	Phe	Tyr	Ala	Ile	Thr	Thr	Leu	His	Asn	Leu	Leu	Leu
215				245						250					255
217	Tyr	Gln	Glu	Gly	Ala	Lys	Met	Ala	Val	Arg	Leu	Ala	Asp	Gly	Leu
218				260						265					270
220	Gln	Lys	Met	Val	Pro	Leu	Leu	Asn	Lys	Asn	Asn	Pro	Lys	Phe	Leu
221				275						280					285
223	Ala	Ile	Thr	Thr	Asp	Cys	Leu	Gln	Leu	Leu	Ala	Tyr	Gly	Asn	Gln
224				290						295					300
226	Glu	Ser	Lys	Leu	Ile	Ile	Leu	Ala	Asn	Gly	Gly	Pro	Gln	Ala	Leu
227				305						310					315
229	Val	Gln	Ile	Met	Arg	Asn	Tyr	Ser	Tyr	Glu	Lys	Leu	Leu	Trp	Thr
230				320						325					330
232	Thr	Ser	Arg	Val	Leu	Lys	Val	Leu	Ser	Val	Cys	Pro	Ser	Asn	Lys
233				335						340					345
235	Pro	Ala	Ile	Val	Glu	Ala	Gly	Gly	Met	Gln	Ala	Leu	Gly	Lys	His
236				350						355					360
238	Leu	Thr	Ser	Asn	Ser	Pro	Arg	Leu	Val	Gln	Asn	Cys	Leu	Trp	Thr
239				365						370					375
241	Leu	Arg	Asn	Leu	Ser	Asp	Val	Ala	Thr	Lys	Gln	Glu	Gly	Leu	Glu

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242		380		385		390
244	Ser Val Leu Lys Ile Leu Val Asn Gln Leu Ser Val Asp Asp Val					
245		395		400		405
247	Asn Val Leu Thr Cys Ala Thr Gly Thr Leu Ser Asn Leu Thr Cys					
248		410		415		420
250	Asn Asn Ser Lys Asn Lys Thr Leu Val Thr Gln Asn Ser Gly Val					
251		425		430		435
253	Glu Ala Leu Ile His Ala Ile Leu Arg Ala Gly Asp Lys Asp Asp					
254		440		445		450
256	Ile Thr Glu Pro Ala Val Cys Ala Leu Arg His Leu Thr Ser Arg					
257		455		460		465
259	His Pro Glu Ala Glu Met Ala Gln Asn Ser Val Arg Leu Asn Tyr					
260		470		475		480
262	Gly Ile Pro Ala Ile Val Lys Leu Leu Asn Gln Pro Asn Gln Trp					
263		485		490		495
265	Pro Leu Val Lys Ala Thr Ile Gly Leu Ile Arg Asn Leu Ala Leu					
266		500		505		510
268	Cys Pro Ala Asn His Ala Pro Leu Gln Glu Ala Ala Val Ile Pro					
269		515		520		525
271	Arg Leu Val Gln Leu Leu Val Lys Ala His Gln Asp Ala Gln Arg					
272		530		535		540
274	His Val Ala Ala Gly Thr Gln Gln Pro Tyr Thr Asp Gly Val Arg					
275		545		550		555
277	Met Glu Glu Ile Val Glu Gly Cys Thr Gly Ala Leu His Ile Leu					
278		560		565		570
280	Ala Arg Asp Pro Met Asn Arg Met Glu Ile Phe Arg Leu Asn Thr					
281		575		580		585
283	Ile Pro Leu Phe Val Gln Leu Leu Tyr Ser Ser Val Glu Asn Ile					
284		590		595		600
286	Gln Arg Val Ala Ala Gly Val Leu Cys Glu Leu Ala Gln Asp Lys					
287		605		610		615
289	Glu Ala Ala Asp Ala Ile Asp Ala Glu Gly Ala Ser Ala Pro Leu					
290		620		625		630
292	Met Glu Leu Leu His Ser Arg Asn Glu Gly Thr Ala Thr Tyr Ala					
293		635		640		645
295	Ala Ala Val Leu Phe Arg Ile Ser Glu Asp Lys Asn Pro Asp Tyr					
296		650		655		660
298	Arg Lys Arg Val Ser Val Glu Leu Thr Asn Ser Leu Phe Lys His					
299		665		670		675
301	Asp Pro Ala Ala Trp Glu Ala Ala Gln Ser Met Ile Pro Ile Asn					
302		680		685		690
304	Glu Pro Tyr Gly Asp Asp Met Asp Ala Thr Tyr Arg Pro Met Tyr					
305		695		700		705
307	Ser Ser Asp Val Pro Leu Asp Pro Leu Glu Met His Met Asp Met					
308		710		715		720
310	Asp Gly Asp Tyr Pro Ile Asp Thr Tyr Ser Asp Gly Leu Arg Pro					
311		725		730		735
313	Pro Tyr Pro Thr Ala Asp His Met Leu Ala					
314		740		745		

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316 <210> SEQ ID NO: 3
317 <211> LENGTH: 1120
318 <212> TYPE: DNA
319 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 3
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324 caagcgggcc aaagccaagg ccaccaagaa gcggccacag cgggccacat 100
326 ccaatgtctt cgcaatgttt gaccagtccc agatccagga gtttaaggag 150
328 gctttcaaca tgattgacca gaaccgtgat ggcttcattg acaaggagga 200
330 cctgcacgac atgctggcct cgctggggaa gaacccaca gacgaatacc 250
332 tggagggcat gatgagcgag gcccggggc catacaactt caccatgttc 300
334 ctccacatgt ttggggagaa gctgaacggc acggaccccg aggatgtgat 350
336 tcgcaacgcc tttgcctgct tcgacgagga atcctcaggt ttcacacatg 400
338 aggaccacct ccggaagctg ctccacca ca tgggtgaccg cttcacagat 450
340 gaggaagtgg acgagatgta ccgggaggca cccgttgata agaaaggcaa 500
342 cttcaactac gtggagttca cccgcattct caaacatggc gccaaaggata 550
344 aacacgacta ggccatcccc agccccctga caccagccc ccgccagtca 600
346 cccctccccg cacacaccgg tccataccag ctccctgccc atgaccctcg 650
348 ctgagggatc cccctttgag ggttagggc ccagttccca gtggaagaaa 700
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356 tccggggctg ttccccgagg aggaagggaa gcctctgtgt gccccccagg 900
358 aggaagaggc cctgagtcct gggatcagac accccttcac gtgtatccca 950
360 cacaaatgca agctcaccaa ggtccctctc cagtccctt cctacaccc 1000
362 tgacgccaga tgccgcacac ccaacgccac cagccatggg agtgtgctca 1050
364 ggagtcgcgg ggcagacgtg acatctgtcc agaggggggca gaatctccaa 1100
366 tagaggactg agacaacatg 1120
368 <210> SEQ ID NO: 4
369 <211> LENGTH: 172
370 <212> TYPE: PRT
371 <213> ORGANISM: Homo sapiens
373 <400> SEQUENCE: 4
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378 20 25 30
380 Ile Gln Glu Phe Lys Glu Ala Phe Asn Met Ile Asp Gln Asn Arg
381 35 40 45
383 Asp Gly Phe Ile Asp Lys Glu Asp Leu His Asp Met Leu Ala Ser
384 50 55 60
386 Leu Gly Lys Asn Pro Thr Asp Glu Tyr Leu Glu Gly Met Met Ser
387 65 70 75
389 Glu Ala Pro Gly Pro Tyr Asn Phe Thr Met Phe Leu Thr Met Phe
390 80 85 90
392 Gly Glu Lys Leu Asn Gly Thr Asp Pro Glu Asp Val Ile Arg Asn
393 95 100 105
395 Ala Phe Ala Cys Phe Asp Glu Glu Ser Ser Gly Phe Ile His Glu
396 110 115 120

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 02/09/2006  
PATENT APPLICATION: US/10/529,349      TIME: 12:31:09

Input Set : A:\P1988R1 Sequence Listing.txt  
Output Set: N:\CRF4\02012006\J529349.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 2298

Seq#:39; N Pos. 34

Seq#:40; Xaa Pos. 11

**VERIFICATION SUMMARY**

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L:2881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:2250

L:4157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0

L:4201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0